

CLAIMS

1. Apparatus for analysing a polynucleotide sequence,
5 comprising a support and attached to a surface thereof an array of
the whole or a chosen part of a complete set of oligonucleotides of
chosen lengths, the different oligonucleotides occupying separate
cells of the array and being capable of taking part in
hybridisation reactions.
- 10 2. Apparatus for studying differences between polynucleotide
sequences, comprising a support and attached to a surface thereof
an array of the whole or a chosen part of a complete set of
oligonucleotides of chosen lengths comprising the polynucleotide
sequences, the different oligonucleotides occupying separate cells
15 of the array and being capable of taking part in hybridisation
reactions.
3. Apparatus as claimed in claim 2, wherein the array
comprises one or more pairs of oligonucleotides of chosen lengths.
4. Apparatus as claimed in claim 3, wherein the array
20 comprises one or more pairs of oligonucleotides of chosen lengths
representing normal and mutant versions of a point mutation to be
studied.
5. Apparatus as claimed in any one of claims 1 or 2, wherein
the chosen length is from 8 to 20 nucleotides.
- 25 6. Apparatus as claimed in any one of claims 1 or 2, wherein
the surface of the support to which the oligonucleotides are
attached is of glass.
7. Apparatus as claimed in any one of claims 1 or 2, wherein
each oligonucleotide is bound to the support through a covalent
30 link.
8. A method of analysing a polynucleotide sequence, by the
use of a support to the surface of which is attached an array of
the whole or a chosen part of a complete set of oligonucleotides of
chosen lengths, the different oligonucleotides occupying separate
35 cells of the array, which method comprises labelling the
polynucleotide sequence or fragments thereof to form labelled
material,

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applying the labelled material under hybridisation conditions to the array, and observing the location of the label on the surface associated with particular members of the set of oligonucleotides.

- 5 9. A method according to claim 8, applied to the study of differences between polynucleotide sequences, wherein the array is of the whole or a chosen part of the complete set of oligonucleotides of chosen lengths comprising the polynucleotide sequences.
- 10 10. A method as claimed in claim 9, wherein the array comprises one or more pairs of oligonucleotides of chosen lengths.
11. A method as claimed in claim 10, wherein the array comprises one or more pairs of oligonucleotides of
- 15 chosen lengths representing normal and mutant versions of a point mutation being studied.
12. A method according to any one of claims 8 to 11, wherein the polynucleotide sequence is randomly degraded to form a mixture of oligomers of a chosen
- 20 length, the mixture being thereafter labelled to form the labelled material.
13. A method as claimed in claim 12, wherein the oligomers are labelled with ³²P.
14. A method as claimed in any one of claims 8 to 11,
- 25 wherein the chosen length is from 8 to 20 nucleotides.
15. A method as claimed in claim 8, where the set of oligonucleotides is attached to the surface as an array of parallel stripes, and at least two polynucleotide sequences are analysed simultaneously by applying the
- 30 labelled material to the array in the form of separate stripes orthogonal to the oligonucleotide stripes.
16. A method as claimed in claim 8, wherein hybridisation is effected in the presence of tetramethylammoniumchloride at a concentration of 1M to
- 35 5M.

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